

01/11

APPROVED	Q. Q. FIG.
BY	CLASS. JCG/ASS
DRAFTSMAN	



FIG. 1

02/11

APPROVED	FIG.
BY	DATE
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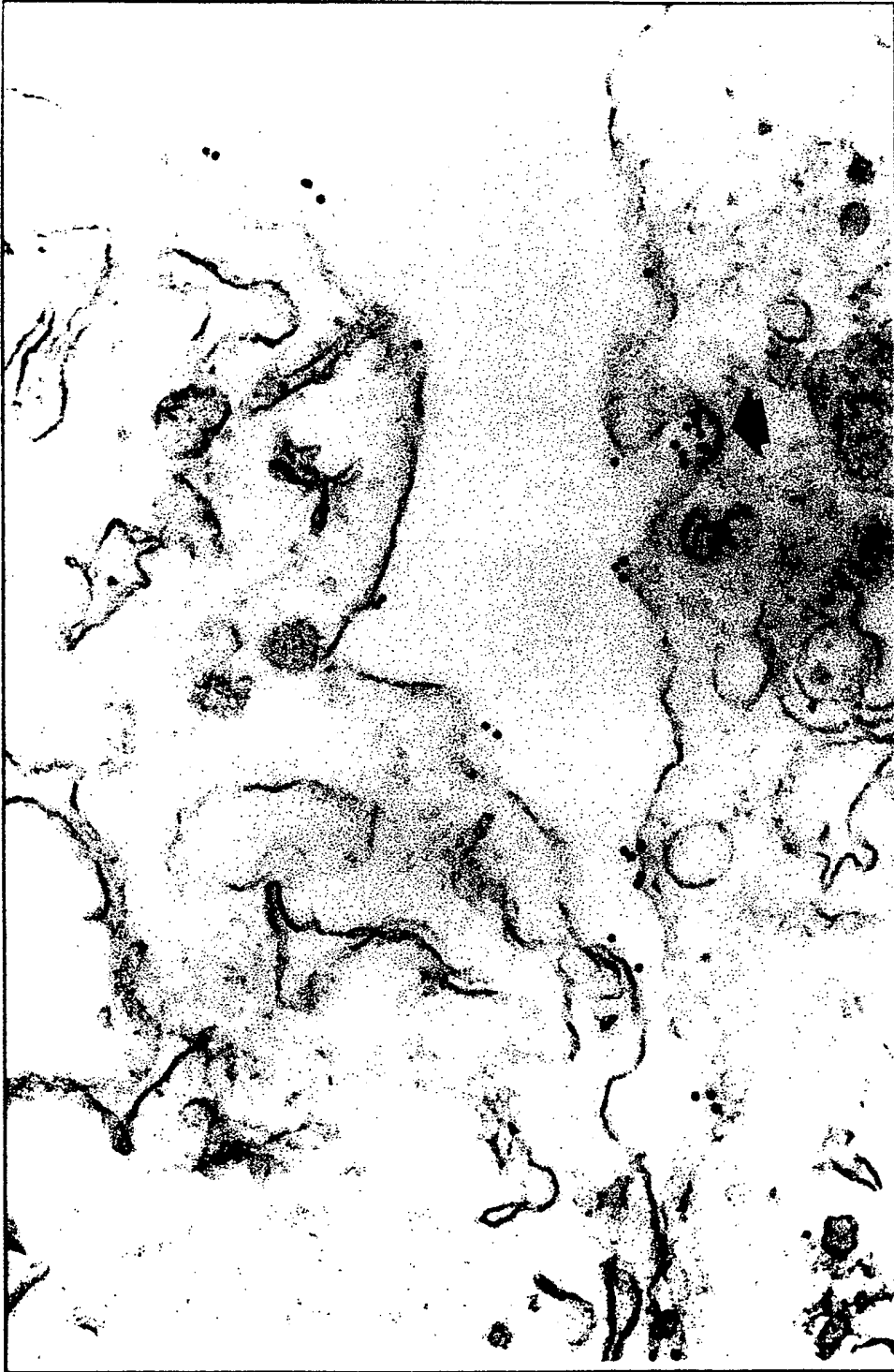


FIG. 2

03/11

APPROVED	FIG.
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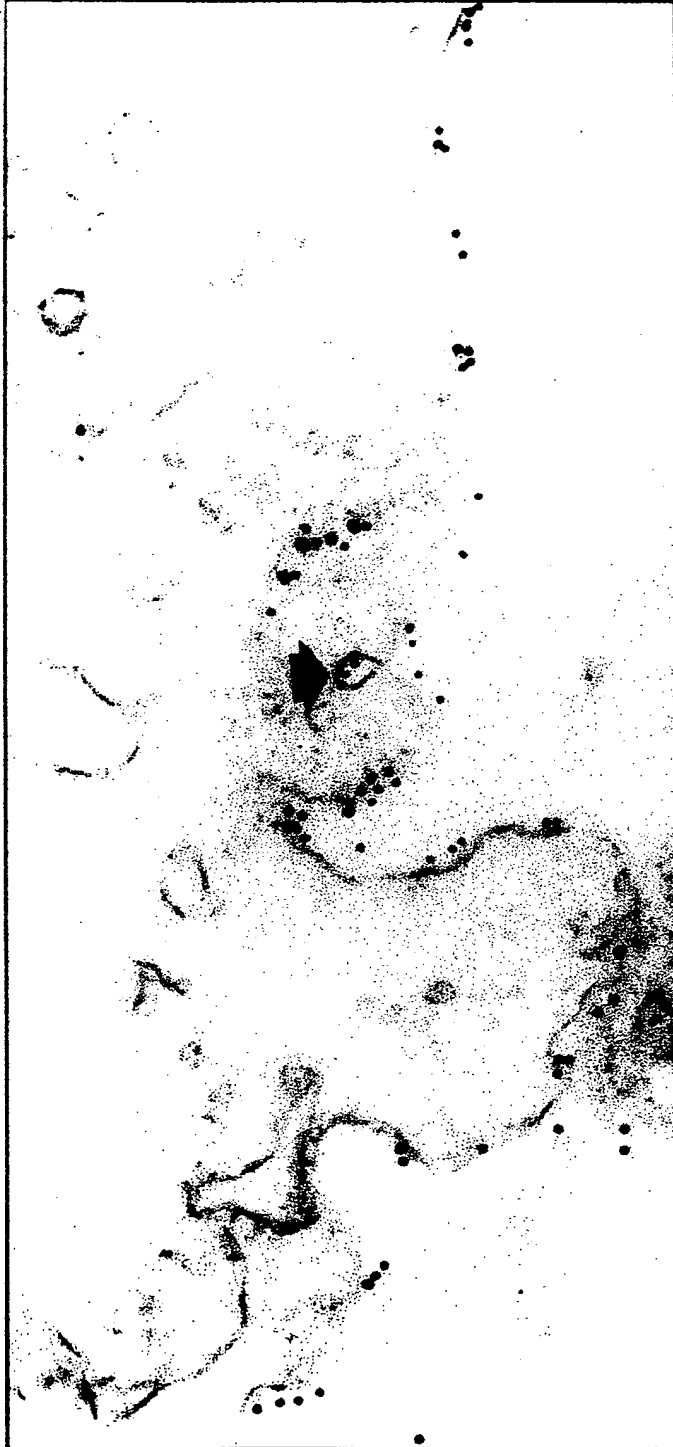


FIG. 3

04/11

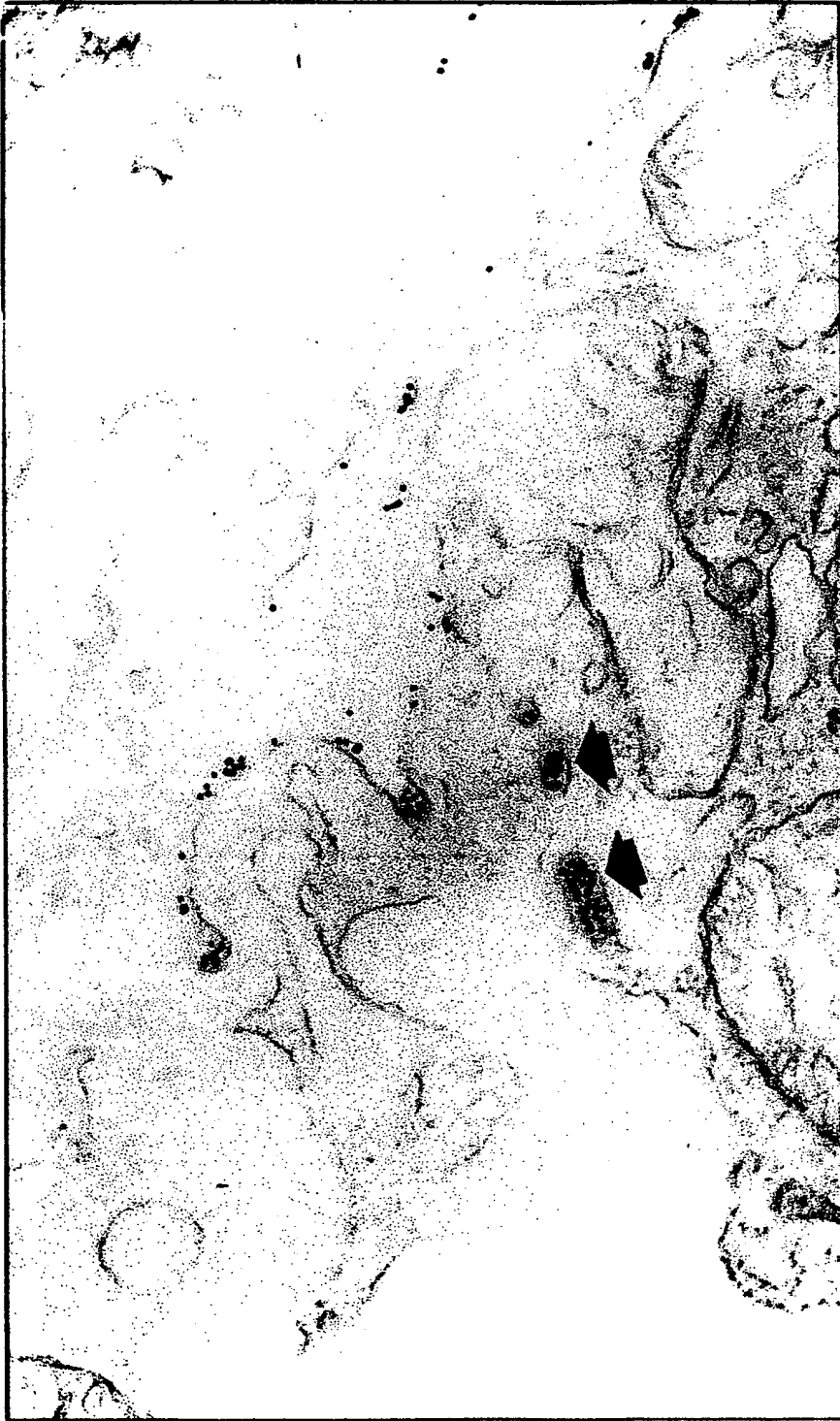


FIG. 4

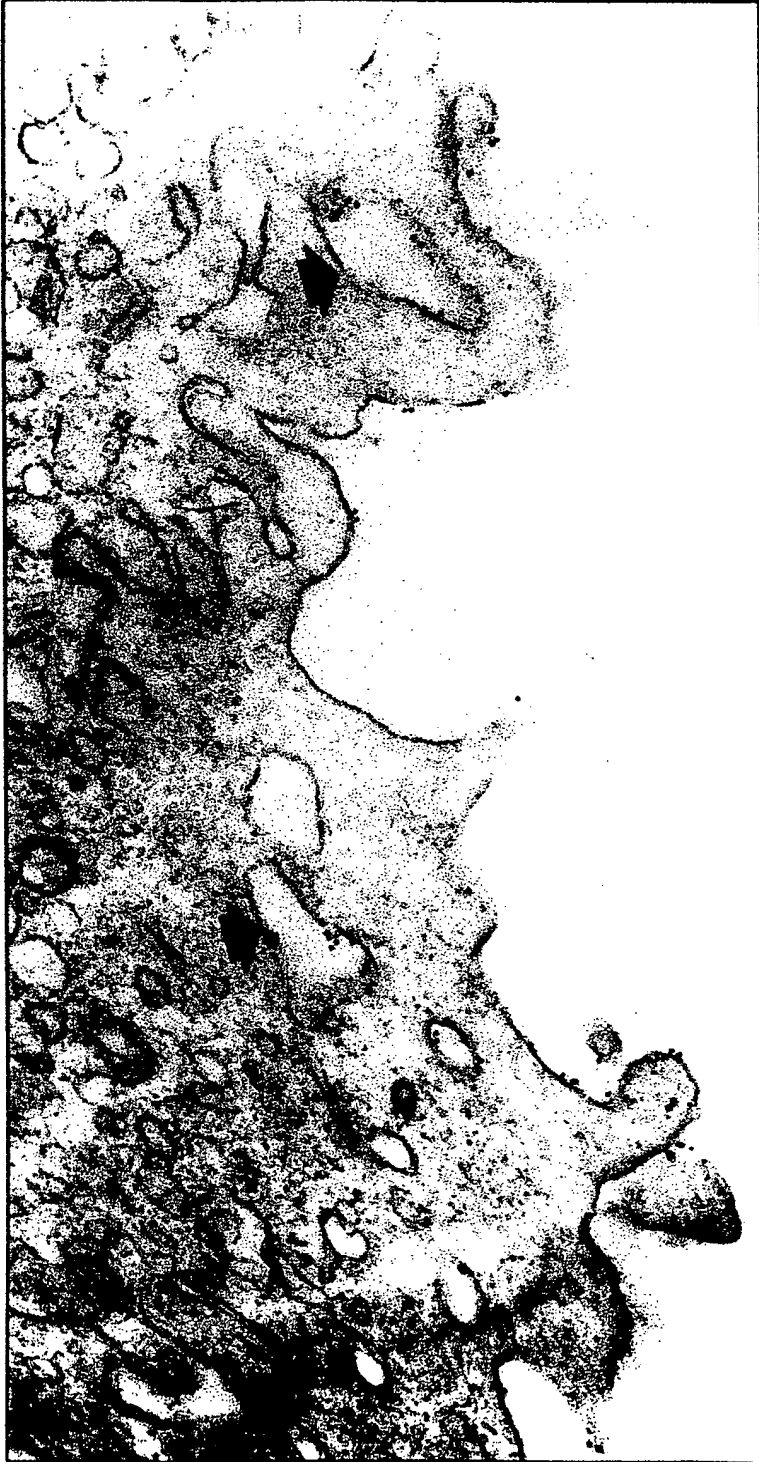
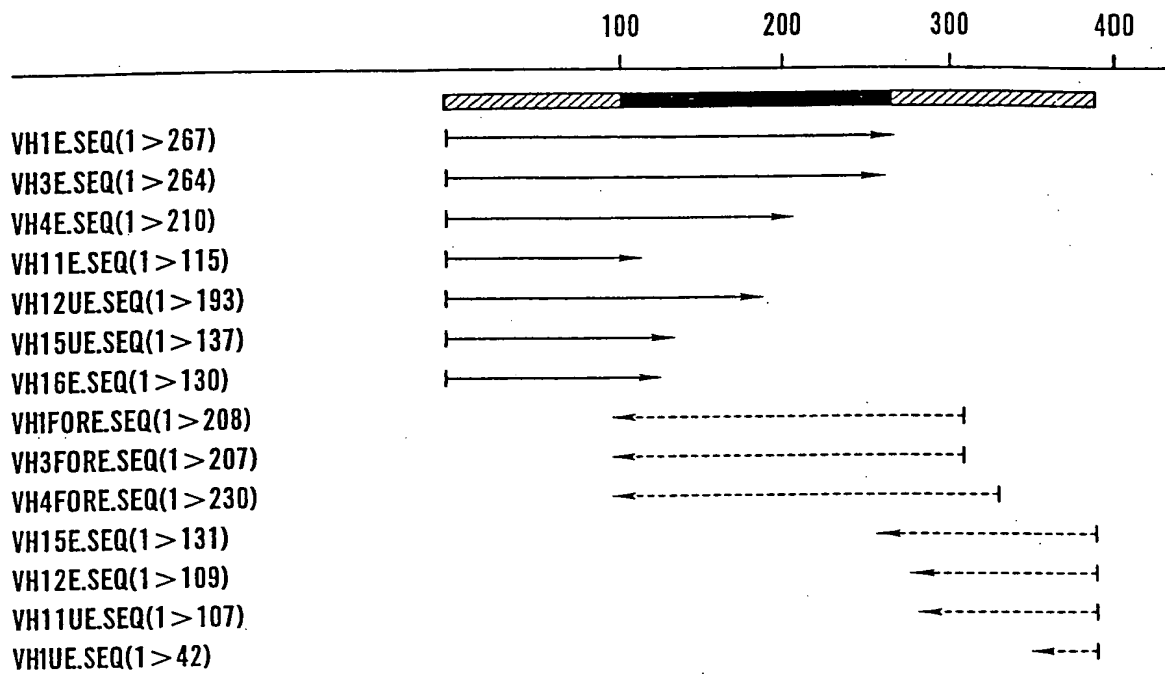


FIG. 5

06/11

APPROVED	Q.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

**FIG. 6**

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/357,704

07/11

ENZYMES: ALL 74 ENZYMES (NO FILTER)

SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

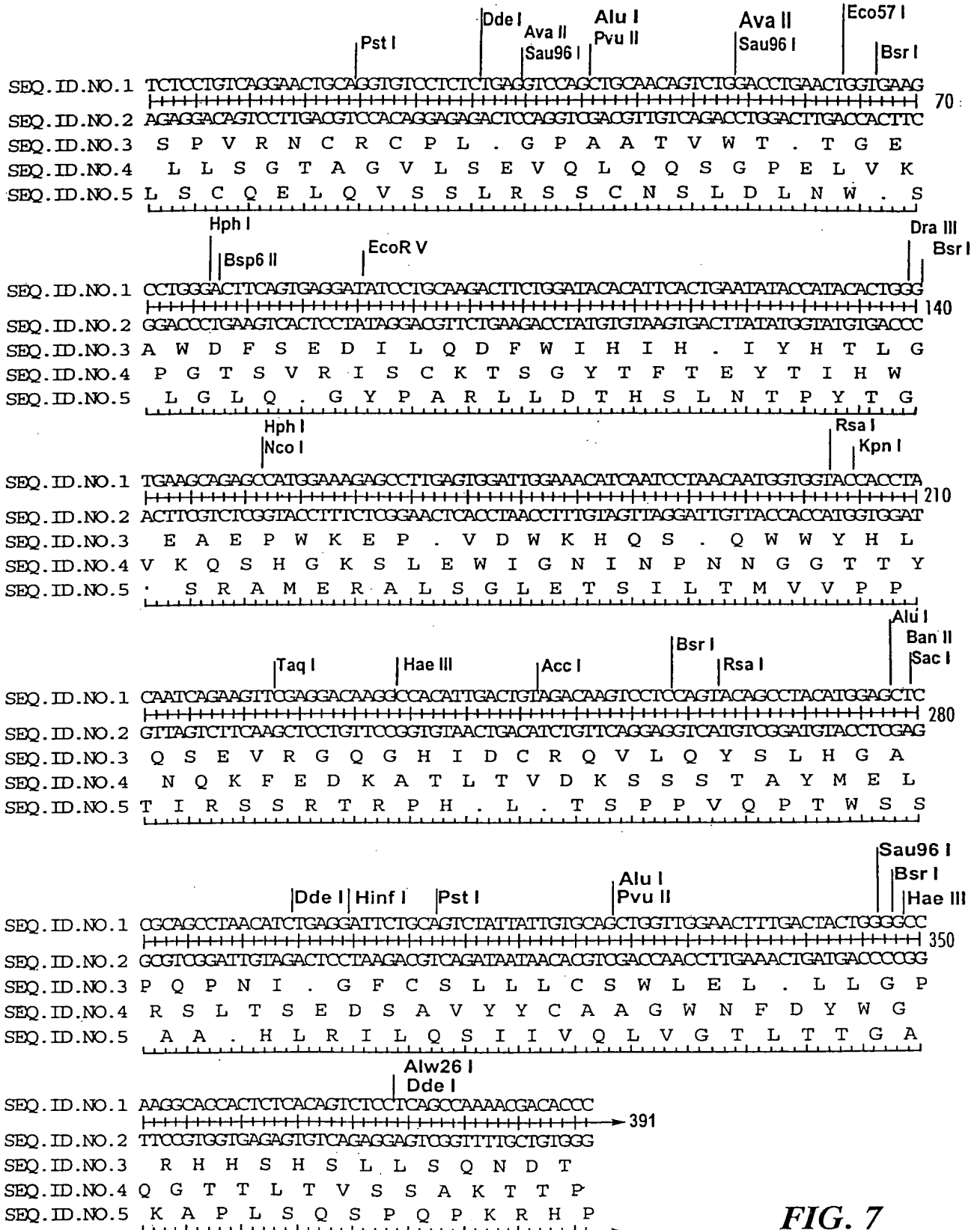
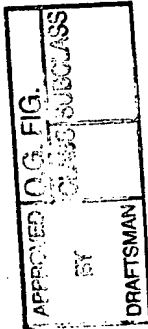


FIG. 7

08/11

APPROVED	Q. G. FIG.
BY	CLASS SUBCLASS
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LIPMAN-PEARSON PROTEIN ALIGNMENT KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115)	SEQ2(1>125)	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
J591VH.PRO	MUVHIIA.PRO				
(1>115)	(1>125)	75.6	2	10	125

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      ↓10      ↓20      ↓30      ↓40      ↓50
EVQLQQSGPELVKPGTSVRISCKTSGYTFTEYTI-HWVKQSHGKSLEWIGNINPNNGGIT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFTDYIMNHWKQSPGKSLEWIGDINPGNGGTS
      ↑10      ↑20      ↑30      ↑40      ↑50      ↑60
↓60      ↓70      ↓80      ↓90      ↓100      ↓110
YNQKFEDKATLTVDKSSSTAYMEIRSLTSEDSAVYYCAAG-----WNFDYWGGGIT
YNQKF.:KATLTVDKSSSTAYM:L.SLTSEDSAVYYCA G      ..FDYWGGGIT
YNQKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGIT
      ↑70      ↑80      ↑90      ↑100      ↑110      ↑120

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LTVSS

:TVSS

VIVSS

FIG. 8

TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

SN: 09/357,704

09/11

APPROVED	Q. Q. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

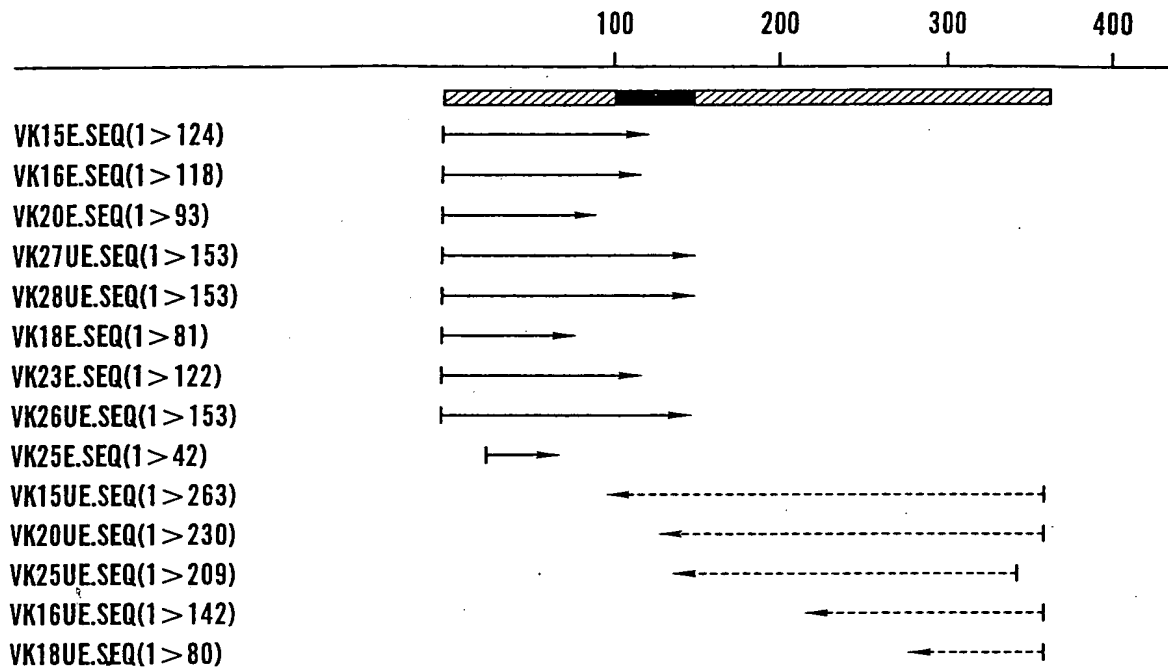


FIG. 9

10/11

ENZYMES: ALL 74 ENZYMES (NO FILTER):
SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

APPROVED	Q. Q. FIG.
BY	CLASS/RECLASS
DRAFTSMAN	

Alu Hph I

SEQ.ID.NO.9 TTATATGGAGCTGATGGGAACATTGTAATGACCCAATCTCCAAATCCATGTCCATGTTCAGTAGGAGAGA 70
SEQ.ID.NO.10 AATATACCTCGACTACCTTGTAACTTACTGGGTAGAGGTTTAGGTACAGGTACAGTCATCCTCTCT
SEQ.ID.NO.11 L Y G A D G N I V M T Q S P K S M S M S V G E
SEQ.ID.NO.12 Y M E L M G T L . . P N L P N P C P C Q . E R
SEQ.ID.NO.13 I I W S . W E H C N D P I S Q I H V H V S R R E

Hae III Bsr I

SEQ.ID.NO.9 GGGTCACCTTGACCTGCAAGGCCAGTGAAGTGTGGTTACTTATGTTTCTGGTATCAACAGAAACCAGA 140
SEQ.ID.NO.10 CCCAGTGGAACTGGAAGTTCGGGTCACTCTTACACCAATGAATACAAAGGACCATAGTTGTCTTTGGTCT
SEQ.ID.NO.11 R V T L T C K A S E N V V T Y V S W Y Q Q K P E
SEQ.ID.NO.12 G S P . P A R P V R M W L L M F P G I N R N Q
SEQ.ID.NO.13 G H L D L Q G Q . E C G Y L C F L V S T E T R

Alw26 I Fok I Hpa II Rsa I Ava II Bsr I Mbo I Dpn I Bsa0 I Pvu I

SEQ.ID.NO.9 GCAGTCTCCTAAACTGCTGATATACGGGCATCCAAACCGTACACTGGGGTCCCGATCGCTTCACAGGC 210
SEQ.ID.NO.10 CGTCAGAGGATTTCAGGACTATATGCCCCGTTAGGTTGGCCATGTGACCCAGGGGCTAGCGAAGTGTCCG
SEQ.ID.NO.11 Q S P K L L I Y G A S N R Y T G V P D R F T G
SEQ.ID.NO.12 S S L L N C . Y T G H P T G T L G S P I A S Q A
SEQ.ID.NO.13 A V S . T A D I R G I Q P V H W G P R S L H R

Mbo I Dpn I Bsp6 II Mbo II Eco57 I

SEQ.ID.NO.9 AGTGGATCTGCAACAGATTTCCTCTGACCATCAGCAGTGTGAGGCTGAAGACCTTGCAGATTATCACT 280
SEQ.ID.NO.10 TCACCTAGACGTGTCTAAAGTGAGACTGGTAGTGTGACACGTCGACTTCTGGAACGTCTAATAGTCA
SEQ.ID.NO.11 S G S A T D F T L T I S S V Q A E D L A D Y H
SEQ.ID.NO.12 V D L Q Q I S L . P S A V C R L K T L Q I I T
SEQ.ID.NO.13 Q W I C N R F H S D H Q Q C A G . R P C R L S L

Alu I Rsa I Ava II Sau96 I Alu I

SEQ.ID.NO.9 GTGGACAGGGTTACAGCTATCCGTACACGTTGGAGGGGGACCAAGCTGGAAATAAAACGGGGCTGATGC 350
SEQ.ID.NO.10 CACCTGTCCAATGTGATAGGCATGTGCAAGCCTCCCCCTGGTTCGACCTTTATTTTGGCCGACTAGC
SEQ.ID.NO.11 C G Q G Y S Y P Y T F G G G T K L E I K R A D A
SEQ.ID.NO.12 V D R V T A I R T R S E G G P S W K . N G L M
SEQ.ID.NO.13 W T G L Q L S V H V R R G D Q A G N K T G . C

SEQ.ID.NO.9 TGCACCAACTGTA
+++++> 363
SEQ.ID.NO.10 ACGTGGTTGACAT
SEQ.ID.NO.11 A P T V
SEQ.ID.NO.12 L H Q L Y
SEQ.ID.NO.13 C T N C
+++++>

FIG. 10

11/11

APPROVED	Q.Q. FIG.
BY	CLASS
DRAFTSMAN	

LIPMAN-PEARSON PROTEIN ALIGNMENT
KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107) J591VK.PRO	SEQ2(1 > 1 1 1) MUVKV.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>107)	(1>109)	60.4	2	2	109

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      ↓10      ↓20      ↓30      ↓40      ↓50
NIVMTQSPKSMMSGVGERVILTCKAS-ENVVTYVSWYQOKPEQSPKLLIYGASNRYTGVP
:I MTQSP.S:S S:G:RVT:TC:AS ::: .Y::WYQOKP. SPKLLIY AS. .:GVP
DIQMTQSPSSLSASLGDRVTITCRASQDDISNYLNWYQOKPGGSPKLLIYYASRLHSGVP
      ↑10      ↑20      ↑30      ↑40      ↑50      ↑60

      ↓60      ↓70      ↓80      ↓90      ↓100
DRFTGSGSATDFTLTISVQAEDLADYHCGQGYSY-PYTFGGGKLEIK
.RF:GSGS:TD::LTIS:::ED:A.Y C QG : P TFGGGKLEIK
SRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNLPPRTFGGGKLEIK
      ↑70      ↑80      ↑90      ↑100

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FIG. 11